

SYR-EPHA2-5001-C1.ST25  
SEQUENCE LISTING

<110> Syrrx, Inc.  
 <120> CRYSTALLIZATION OF EPHRIN RECEPTOR A2  
 <130> SYR-EPHA2-5001-C1  
 <140> Not Yet Assigned  
 <141> 2003-06-20  
 <150> 60/390,356  
 <151> 2002-06-21  
 <160> 3  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 976  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> Amino acid sequence for full length human wild type EPHA2  
 <222> (1)..(976)  
 <223>  
 <220>  
 <221> Amino acid sequence for full length human wild type EPHA2  
 <222> (1)..(976)  
 <223> SEQ. ID. No. 1 encodes for residues 596-900  
 <300>  
 <308> GenBank Accession No. M59371  
 <309> 1994-11-21  
 <313> (1)..(976)  
 <400> 1  
 Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys  
 1 5 10 15  
 Ala Leu Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu  
 20 25 30  
 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr  
 35 40 45  
 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile  
 50 55 60  
 Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp  
 65 70 75 80  
 Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Asn Asn Phe  
 85 90 95

SYR-EPHA2-5001-C1.ST25

Glu Leu Asn Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala  
100 105 110

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu  
115 120 125

Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr  
130 135 140

Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His  
145 150 155 160

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys  
165 170 175

Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu  
180 185 190

Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu  
195 200 205

Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala  
210 215 220

Thr Val Ala Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly  
225 230 235 240

Glu Glu Pro Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro  
245 250 255

Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala  
260 265 270

Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser  
275 280 285

Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala  
290 295 300

Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro  
305 310 315 320

Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr  
325 330 335

Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln

SYR-EPHA2-5001-C1.ST25

340

345

350

Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln  
355 360 365

Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg  
370 375 380

Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser  
385 390 395 400

Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn  
405 410 415

Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val  
420 425 430

Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser  
435 440 445

Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser  
450 455 460

Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn  
465 470 475 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp  
485 490 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln  
500 505 510

Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser  
515 520 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly  
530 535 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg  
545 550 555 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe  
565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His  
580 585 590

## SYR-EPHA2-5001-C1.ST25

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile  
595 600 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe  
610 615 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu  
625 630 635 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln  
645 650 655

Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His  
660 665 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met  
675 680 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu  
690 695 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu  
705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val  
725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val  
740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro  
755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr  
770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
835 840 845

SYR-EPHA2-5001-C1.ST25

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe  
850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser  
865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro  
885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp  
900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala  
915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile  
930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr  
945 950 955 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
965 970 975

<210> 2  
<211> 915  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Human cDNA sequence encoding residues 596-900 of EPHA2  
<222> (1)..(915)  
<223>

<400> 2  
gacccaacc aggcgtgtgtt gaagttcact accgagatcc atccatcctg tgtcactcgg 60  
cagaagggtga tcggagcagg agagtttggg gaggtgtaca agggcatgct gaagacatcc 120  
tcggggaaga aggaggtgcc ggtggccatc aagacgctga aagccggcta cacagagaag 180  
cagcgagtgg acttcctcgg cgaggccggc atcatgggcc agttcagcca ccacaacatc 240  
atccgcctag agggcgatcat ctccaaatac aagcccatga tgatcatcac tgagtacatg 300  
gagaatgggg ccctggacaa gttccttcgg gagaaggatg gcgagttcag cgtgctgcag 360  
ctggtgggca tgctgcgggg catcgagct ggcatagaat acctggccaa catgaactat 420  
gtgcaccgtg acctggctgc ccgcaacatc ctcgtcaaca gcaacctggt ctgcaagggtg 480  
tctgactttg gcctgtcccg cgtgctggag gacgaccccg aggccaccta caccaccagt 540  
ggcggcaaga tccccatccg ctggaccgcc ccggaggcca tttcctaccg gaagttcacc 600

SYR-EPHA2-5001-C1.ST25

tctgccagcg acgtgtggag ctttggcatt gtcattgtggg aggtgatgac ctatggcgag 660  
 cggccctact gggagttgtc caaccacgag gtgatgaaag ccatcaatga tggcttccgg 720  
 ctccccacac ccatggactg cccctccgcc atctaccagc tcatgatgca gtgctggcag 780  
 caggagcgtg cccgccgccc caagttcgct gacatcgta gcatcctgga caagctcatt 840  
 cgtgcccctg actccctcaa gaccctggct gactttgaac cccgcgtgtc tatccggctc 900  
 cccagcacga gcggc 915

<210> 3  
 <211> 333  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> Amino acid sequence for residues 596-900 of EPHA2 with a cleavable (rTev)  
 N-terminal 6x-histidine tag  
 <222> (1)..(333)  
 <223>

<220>  
 <221> Cleavable (rTev) N-terminal 6x-histidine tag  
 <222> (1)..(28)  
 <223>

<400> 3

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr  
 1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Gly Ser Asp Pro Asn Gln  
 20 25 30

Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg  
 35 40 45

Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met  
 50 55 60

Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr  
 65 70 75 80

Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu  
 85 90 95

Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu  
 100 105 110

Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met  
 115 120 125

SYR-EPHA2-5001-C1.ST25

Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe  
 130 135 140  
 Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met  
 145 150 155 160  
 Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg  
 165 170 175  
 Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly  
 180 185 190  
 Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser  
 195 200 205  
 Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr  
 210 215 220  
 Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met  
 225 230 235 240  
 Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn  
 245 250 255  
 His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro  
 260 265 270  
 Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln  
 275 280 285  
 Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu  
 290 295 300  
 Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe  
 305 310 315 320  
 Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly  
 325 330